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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/963,340

DATE: 01/08/2002

TIME: 10:35:29

Input Set : N:\Crf3\RULE60\09963340.raw

Output Set: N:\CRF3\01082002\I963340.raw

1 <110> APPLICANT: Conkling, Mark
 2 Mendu, Nandini
 3 Song, Wen
 4 <120> TITLE OF INVENTION: Regulation of Quinolinate Phosphoribosyl Transferase
 5 Expression
 6 <130> FILE REFERENCE: 5051-338
 7 <140> CURRENT APPLICATION NUMBER: US/09/963,340
 8 <141> CURRENT FILING DATE: 2001-09-24
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/021,286
 W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-10
 11 <160> NUMBER OF SEQ ID NOS: 3
 12 <170> SOFTWARE: PatentIn Ver. 2.0
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 1399
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Nicotiana tabacum
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (52)..(1104)
 21 <400> SEQUENCE: 1
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 23 Met Phe
 24 1
 25 aga gct att cct ttc act gct aca gtg cat cct tat gca att aca gct 105
 26 Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala
 27 5 10 15
 28 cca agg ttg gtg gtg aaa atg tca gca ata gcc acc aag aat aca aga 153
 29 Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg
 30 20 25 30
 31 gtg gag tca tta gag gtg aaa cca cca gca cac cca act tat gat tta 201
 32 Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu
 33 35 40 45 50
 34 aag gaa gtt atg aaa ctt gca ctc tct gaa gat gct ggg aat tta gga 249
 35 Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly
 36 55 60 65
 37 gat gtg act tgt aag gcg aca att cct ctt gat atg gaa tcc gat gct 297
 38 Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala
 39 70 75 80
 40 cat ttt cta gca aag gaa gac ggg atc ata gca gga att gca ctt gct 345
 41 His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala
 42 85 90 95
 43 gag atg ata ttc gcg gaa gtt gat cct tca tta aag gtg gag tgg tat 393
 44 Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr
 45 100 105 110
 46 gta aat gat ggc gat aaa gtt cat aaa ggc ttg aaa ttt ggc aaa gta 441
 47 Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val
 48 115 120 125 130

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49   caa gga aac gct tac aac att gtt ata gct gag agg gtt gtt ctc aat 489
50   Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn
51           135           140           145
52   ttt atg caa aga atg agt gga ata gct aca cta act aag gaa atg gca 537
53   Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala
54           150           155           160
55   gat gct gca cac cct gct tac atc ttg gag act agg aaa act gct cct 585
56   Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro
57           165           170           175
58   gga tta cgt ttg gtg gat aaa tgg gcg gta ttg atc ggt ggg ggg aag 633
59   Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys
60           180           185           190
61   aat cac aga atg ggc tta ttt gat atg gta atg ata aaa gac aat cac 681
62   Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His
63           195           200           205           210
64   ata tct gct gct gga ggt gtc ggc aaa gct cta aaa tct gtg gat cag 729
65   Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln
66           215           220           225
67   tat ttg gag caa aat aaa ctt caa ata ggg gtt gag gtt gaa acc agg 777
68   Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg
69           230           235           240
70   aca att gaa gaa gta cgt gag gtt cta gac tat gca tct caa aca aag 825
71   Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys
72           245           250           255
73   act tcg ttg act agg ata atg ctg gac aat atg gtt gtt cca tta tct 873
74   Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser
75           260           265           270
76   aac gga gat att gat gta tcc atg ctt aag gag gct gta gaa ttg atc 921
77   Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile
78           275           280           285           290
79   aat ggg agg ttt gat acg gag gct tca gga aat gtt acc ctt gaa aca 969
80   Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr
81           295           300           305
82   gta cac aag att gga caa act ggt gtt acc tac att tct agt ggt gcc 1017
83   Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala
84           310           315           320
85   ctg acg cat tcc gtg aaa gca ctt gac att tcc ctg aag atc gat aca 1065
86   Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr
87           325           330           335
88   gag ctc gcc ctt gaa gtt gga agg cgt aca aaa cga gca tgagcgccat 1114
89   Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
90           340           345           350
91   tacttctgct ataggggttg agtaaaagca gctgaatagc tgaaagggtgc aaataagaat 1174
92   cattttacta gttgtcaaac aaaagatcct tcactgtgta atcaaacaaa aagatgtaaa 1234
93   ttgctggaat atctcagatg gctcttttcc aaccttattg cttgagttgg taatttcatt 1294
94   atagctttgt tttcatgttt catggaattt gttacaatga aaatacttga tttataagtt 1354
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97 <210> SEQ ID NO: 2
98 <211> LENGTH: 351

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99 <212> TYPE: PRT

100 <213> ORGANISM: Nicotiana tabacum

101 <400> SEQUENCE: 2

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105           20           25           30
106   Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr
107       35           40           45
108   Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn
109       50           55           60
110   Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser
111       65           70           75           80
112   Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala
113           85           90           95
114   Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu
115           100          105          110
116   Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly
117           115          120          125
118   Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val
119           130          135          140
120   Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu
121       145          150          155          160
122   Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr
123           165          170          175
124   Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly
125           180          185          190
126   Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp
127           195          200          205
128   Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val
129       210          215          220
130   Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu
131       225          230          235          240
132   Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln
133           245          250          255
134   Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro
135           260          265          270
136   Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu
137       275          280          285
138   Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu
139       290          295          300
140   Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser
141       305          310          315          320
142   Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile
143           325          330          335
144   Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
145       340          345          350

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147 <210> SEQ ID NO: 3

148 <211> LENGTH: 1053

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149 <212> TYPE: DNA
150 <213> ORGANISM: Nicotiana tabacum
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154   aaaccaccag cacaccaaac ttatgattta aaggaagtta tgaaacttgc actctctgaa 180
155   gatgctggga atttaggaga tgtgacttgt aaggcgacaa ttctcttga tatggaatcc 240
156   gatgctcatt ttctagcaaa ggaagacggg atcatagcag gaattgcact tgctgagatg 300
157   atattcgcgg aagttgatcc ttcattaaag gtggagtggg atgtaaatga tggcgataaa 360
158   gttcataaaag gcttgaaaatt tggcaaagta caaggaaacg cttacaacat tgttatagct 420
159   gagaggggtg ttctcaattt tatgcaaaga atgagtggaa tagctacact aactaaggaa 480
160   atggcagatg ctgcacaccc tgcttacatg ttggagacta ggaaaactgc tcctggatta 540
161   cgtttggtgg ataaatgggc ggtattgatc ggtgggggga agaatacag aatgggctta 600
162   tttgatatgg taatgataaa agacaatcac atatctgctg ctggaggtgt cggcaaagct 660
163   ctaaaatctg tggatcagta tttggagcaa aataaacttc aaataggggt tgaggttgaa 720
164   accaggacaa ttgaagaagt acgtgaggtt ctagactatg catctcaaac aaagacttcg 780
165   ttgactagga taatgctgga caatatggtt gttccattat ctaacggaga tattgatgta 840
166   tccatgctta aggaggctgt agaattgatc aatgggaggt ttgatacgga ggcttcagga 900
167   aatgttaccg ttgaaacagt acacaagatt ggacaaactg gtgttaccta cttttctagt 960
168   ggtgccctga cgcattccgt gaaagcactt gacatttccc tgaagatcga tacagagctc 1020
169   gcccttgaag ttggaaggcg tacaaaacga gca                                     1053

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VERIFICATION SUMMARY

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